

L3 ANSWER 32 OF 33 MEDLINE
 AN 92164659 MEDLINE
 DN 92164659 PubMed ID: 1537343
 TI Identification and characterization of yeast mutants and the gene for a
 cruciform cutting endonuclease.
 AU Kleff S; Kemper B; Sternglanz R
 CS Department of Biochemistry and Cell Biology, SUNY, Stony Brook 11794.
 NC GM28220 (NIGMS)
 SO EMBO JOURNAL, (1992 Feb) 11 (2) 699-704.
 Journal code: EMB; 8208664. ISSN: 0261-4189.
 CY ENGLAND: United Kingdom
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 OS GENBANK-M65275; GENBANK-X60225
 EM 199203
 ED Entered STN: 19920417
 Last Updated on STN: 19920417
 Entered Medline: 19920331
 AB An assay was developed that detected DNA cruciform cutting endonuclease
 activity in crude extracts of *Saccharomyces cerevisiae*. A collection of
 temperature-sensitive strains was screened using this assay, and a mutant
 lacking the activity was found. The mutation leading to the enzymatic
 defect was mapped to the left arm of chromosome XI within 3 **cm**
 of the centromere. Cloning of the gene for this endonuclease was achieved
 by **chromosome walking** from the nearby PUT3 locus. The
 gene, called CCE1 (cruciform cutting endonuclease), was **sequenced**
 and found to have an open reading frame encoding a 41 kDa protein. The
 amino acid **sequence** of this eukaryotic endonuclease shows
 homology neither to its prokaryotic counterparts nor to other proteins in
 available databases. A cce1 null mutant has no obvious growth defect, and
 despite the ability of the CCE1 enzyme to cleave Holliday junction
 analogs, the mutant shows no defect in meiotic or mitotic recombination.
 A second cruciform cutting activity was detected in extracts from a cce1
 null mutant, indicating that yeast has at least two such enzymes. The
 only phenotype observed for cce1 mutants is a higher than normal frequency of
 appearance of petite cells, suggesting that the CCE1 protein is important
 for the maintenance of mitochondrial DNA.

L3 ANSWER 29 OF 33 MEDLINE
 AN 92361255 MEDLINE
 DN 92361255 PubMed ID: 1354004
 TI Effects of ionizing radiation on a plant genome: analysis of two Arabidopsis transparent testa mutations.
 AU Shirley B W; Hanley S; Goodman H M
 CS Department of Genetics, Harvard Medical School, Massachusetts General Hospital, Boston 02114.
 SO PLANT CELL, (1992 Mar) 4 (3) 333-47.
 Journal code: BJU; 9208688. ISSN: 1040-4651.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
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 OS GENBANK-M86358; GENBANK-M86359
 EM 199209
 ED Entered STN: 19920925
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 Entered Medline: 19920914
 AB Ionizing radiation is known to cause chromosomal alterations such as inversions and deletions and has been used extensively for inducing mutations. In Arabidopsis, two methods for the isolation of genes identified on the basis of mutant phenotypes--genomic subtraction and **chromosome walking**--either rely on or are greatly facilitated by the availability of these types of mutations. This article gives a detailed characterization of ionizing radiation-induced mutations in plants. The Arabidopsis genes encoding chalcone flavanone isomerase (CHI) and dihydroflavonol 4-reductase (DFR) were cloned and found to correspond to two transparent testa loci. A CHI allele, generated by fast-neutron irradiation, consisted of an inversion within the gene. A 272-bp fragment from 38 **centimorgans** away on the same chromosome was transferred to one end of this inversion. A DFR allele, induced by x-irradiation, contained two deletions and an inversion of the 2.8-**centimorgan** intervening region. **Sequence** analysis of the break points in both mutants indicate that repair of radiation-induced damage involves mechanisms similar or identical to those that mediate the integration of foreign **sequences** into the genome. The chromosome rearrangements found in these mutants have important implications for the use of ionizing radiation-induced alleles in classical and molecular genetic experiments in plants.